

Sequence Listing

SEQUENCE LISTING

<110> Steinkasserer, Alexander

<120> Use of Soluble Forms of CD83 and Nucleic Acids Encoding them for the Treatment or Prevention of Diseases

<130> 032723woJH

<140>

<141>

<160> 12

<170> PatentIn Ver. 2.1

<210> 1

<211> 618

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1)..(615)

<400> 1

atg tcg cgc ggc ctc cag ctt ctg ctc ctg agc tgc gcc tac agc ctg	48
Met Ser Arg Gly Leu Gln Leu Leu Leu Ser Cys Ala Tyr Ser Leu	
1 5 10 15	
gct ccc gcg acg ccg gag gtg aag gtg gct tgc tcc gaa gat gtg gac	96
Ala Pro Ala Thr Pro Glu Val Lys Val Ala Cys Ser Glu Asp Val Asp	
20 25 30	
ttg ccc tgc acc gcc ccc tgg gat ccg cag gtt ccc tac acg gtc tcc	144
Leu Pro Cys Thr Ala Pro Trp Asp Pro Gln Val Pro Tyr Thr Val Ser	
35 40 45	
tgg gtc aag tta ttg gag ggt ggt gaa gag agg atg gag aca ccc cag	192
Trp Val Lys Leu Leu Glu Gly Gly Glu Glu Arg Met Glu Thr Pro Gln	
50 55 60	
gaa gac cac ctc agg gga cag cac tat cat cag aag ggg caa aat ggt	240
Glu Asp His Leu Arg Gly Gln His Tyr His Gln Lys Gly Gln Asn Gly	
65 70 75 80	
tct ttc gac gcc ccc aat gaa agg ccc tat tcc ctg aag atc cga aac	288
Ser Phe Asp Ala Pro Asn Glu Arg Pro Tyr Ser Leu Lys Ile Arg Asn	
85 90 95	
act acc agc tgc aac tcg ggg aca tac agg tgc act ctg cag gac ccg	336
Thr Thr Ser Cys Asn Ser Gly Thr Tyr Arg Cys Thr Leu Gln Asp Pro	
100 105 110	
gat ggg cag aga aac cta agt ggc aag gtg atc ttg aga gtg aca gga	384
Asp Gly Gln Arg Asn Leu Ser Gly Lys Val Ile Leu Arg Val Thr Gly	
115 120 125	
tgc cct gca cag cgt aaa gaa gag act ttt aag aaa tac aga gcg gag	432
Cys Pro Ala Gln Arg Lys Glu Glu Thr Phe Lys Lys Tyr Arg Ala Glu	
130 135 140	
att gtc ctg ctg ctg gct ctg gtt att ttc tac tta aca ctc atc att	480
Ile Val Leu Leu Leu Ala Leu Val Ile Phe Tyr Leu Thr Leu Ile Ile	
145 150 155 160	
ttc act tgt aag ttt gca cgg cta cag agt atc ttc cca gat ttt tct	528

Sequence Listing

Phe Thr Cys Lys Phe Ala Arg Leu Gln Ser Ile Phe Pro Asp Phe Ser
 165 170 175
 aaa gct ggc atg gaa cga gct ttt ctc cca gtt acc tcc cca aat aag 576
 Lys Ala Gly Met Glu Arg Ala Phe Leu Pro Val Thr Ser Pro Asn Lys
 180 185 190
 cat tta ggg cta gtg act cct cac aag aca gaa ctg gta tga 618
 His Leu Gly Leu Val Thr Pro His Lys Thr Glu Leu Val
 195 200 205

<210> 2
 <211> 205
 <212> PRT
 <213> Homo sapiens

<400> 2
 Met Ser Arg Gly Leu Gln Leu Leu Leu Leu Ser Cys Ala Tyr Ser Leu
 1 5 10 15
 Ala Pro Ala Thr Pro Glu Val Lys Val Ala Cys Ser Glu Asp Val Asp
 20 25 30
 Leu Pro Cys Thr Ala Pro Trp Asp Pro Gln Val Pro Tyr Thr Val Ser
 35 40 45
 Trp Val Lys Leu Leu Glu Gly Gly Glu Glu Arg Met Glu Thr Pro Gln
 50 55 60
 Glu Asp His Leu Arg Gly Gln His Tyr His Gln Lys Gly Gln Asn Gly
 65 70 75 80
 Ser Phe Asp Ala Pro Asn Glu Arg Pro Tyr Ser Leu Lys Ile Arg Asn
 85 90 95
 Thr Thr Ser Cys Asn Ser Gly Thr Tyr Arg Cys Thr Leu Gln Asp Pro
 100 105 110
 Asp Gly Gln Arg Asn Leu Ser Gly Lys Val Ile Leu Arg Val Thr Gly
 115 120 125
 Cys Pro Ala Gln Arg Lys Glu Glu Thr Phe Lys Lys Tyr Arg Ala Glu
 130 135 140
 Ile Val Leu Leu Leu Ala Leu Val Ile Phe Tyr Leu Thr Leu Ile Ile
 145 150 155 160
 Phe Thr Cys Lys Phe Ala Arg Leu Gln Ser Ile Phe Pro Asp Phe Ser
 165 170 175
 Lys Ala Gly Met Glu Arg Ala Phe Leu Pro Val Thr Ser Pro Asn Lys
 180 185 190
 His Leu Gly Leu Val Thr Pro His Lys Thr Glu Leu Val
 195 200 205

<210> 3
 <211> 2051
 <212> DNA
 <213> Mus musculus
 <220>

Sequence Listing

<221> CDS

<222> (14)..(601)

<400> 3

```

gcgctccagc cgc atg tgc caa ggc ctc cag ctc ctg ttt cta ggc tgc 49
      Met Ser Gln Gly Leu Gln Leu Leu Phe Leu Gly Cys
      1          5          10

gcc tgc agc ctg gca ccc gcg atg gcg atg cgg gag gtg acg gtg gct 97
Ala Cys Ser Leu Ala Pro Ala Met Ala Met Arg Glu Val Thr Val Ala
      15          20          25

tgc tcc gag acc gcc gac ttg cct tgc aca gcg ccc tgg gac ccg cag 145
Cys Ser Glu Thr Ala Asp Leu Pro Cys Thr Ala Pro Trp Asp Pro Gln
      30          35          40

ctc tcc tat gca gtg tcc tgg gcc aag gtc tcc gag agt ggc act gag 193
Leu Ser Tyr Ala Val Ser Trp Ala Lys Val Ser Glu Ser Gly Thr Glu
      45          50          55

agt gtg gag ctc ccg gag agc aag caa aac agc tcc ttc gag gcc ccc 241
Ser Val Glu Leu Pro Glu Ser Lys Gln Asn Ser Ser Phe Glu Ala Pro
      65          70          75

agg aga agg gcc tat tcc ctg acg atc caa aac act acc atc tgc agc 289
Arg Arg Arg Ala Tyr Ser Leu Thr Ile Gln Asn Thr Thr Ile Cys Ser
      80          85          90

tcg ggc acc tac agg tgt gcc ctg cag gag ctc gga ggg cag cgc aac 337
Ser Gly Thr Tyr Arg Cys Ala Leu Gln Glu Leu Gly Gly Gln Arg Asn
      95          100          105

ttg agc ggc acc gtg gtt ctg aag gtg aca gga tgc ccc aag gaa gct 385
Leu Ser Gly Thr Val Val Leu Lys Val Thr Gly Cys Pro Lys Glu Ala
      110          115          120

aca gag tca act ttc agg aag tac agg gca gaa gct gtg ttg ctc ttc 433
Thr Glu Ser Thr Phe Arg Lys Tyr Arg Ala Glu Ala Val Leu Leu Phe
      125          130          135

tct ctg gtt gtt ttc tac ctg aca ctc atc att ttc acc tgc aaa ttt 481
Ser Leu Val Val Phe Tyr Leu Thr Leu Ile Ile Phe Thr Cys Lys Phe
      145          150          155

gca cga cta caa agc att ttc cca gat att tct aaa cct ggt acg gaa 529
Ala Arg Leu Gln Ser Ile Phe Pro Asp Ile Ser Lys Pro Gly Thr Glu
      160          165          170

caa gct ttt ctt cca gtc acc tcc cca agc aaa cat ttg ggg cca gtg 577
Gln Ala Phe Leu Pro Val Thr Ser Pro Ser Ser Lys His Leu Gly Pro Val
      175          180          185

acc ctt cct aag aca gaa acg gta tgagtaggat ctccactggt ttttacaag 631
Thr Leu Pro Lys Thr Glu Thr Val
      190          195

ccaagggcac atcagatcag tgtgcctgaa tgccacccgg acaagagaag aatgagctcc 691

atcctcagat ggcaaccttt ctttgaagtc cttcacctga cagtgggctc cacactactc 751

cctgacacag ggtcttgagc accatcatat gatcacgaag catggagtat caccgcttct 811

```

Sequence Listing

ctgtggctgt cagcttaatg tttcatgtgg ctatctggtc aacctcgtga gtgcttttca 871
gtcatctaca agctatggtg agatgcaggt gaagcagggg catgggaaat ttgaacactc 931
tgagctggcc ctgtgacaga ctctgagga cagctgtcct ctctacatc tgggatacat 991
ctctttgaat ttgtcctgtt tcgttgacc agcccagatg tctcacatct ggcggaaatt 1051
gacaggccaa gctgtgagcc agtgggaaat atttagcaaa taatttccca gtgcgaaggt 1111
cctgctatta gtaaggagta ttatgtgtac atagaaatga gaggtcagtg aactattccc 1171
cagcagggcc ttttcatctg gaaaagacat ccacaaaagc agcaatacag agggatgccca 1231
catttatttt tttaatcttc atgtacttgt caaagaagaa tttttcatgt tttttcaaag 1291
aagtgtgttt ctttcctttt ttaaaatatg aagggtctagt tacatagcat tgctagctga 1351
caagcagcct gagagaagat ggagaatggt cctcaaaata gggacagcaa gctagaagca 1411
ctgtacagtg ccctgctggg aagggcagac aatggactga gaaaccagaa gtctggccac 1471
aagattgtct gtatgattct ggacgagtca cttgtgggtt tcaactctctg gttagtaaac 1531
cagatagttt agtctgggtt gaatacaatg gatgtgaagt tgcttgggga aagctgaatg 1591
tagtgaatac attggcaact ctactgggct gttaccttgt tgatataccta gagttctgga 1651
gctgagcgaa tgcctgtcat atctcagctt gcccatcaat ccaaacacag gaggctacaa 1711
aaaggacatg agcatggtct tctgtgtgaa ctctcctga gaaacgtgga gactggctca 1771
gcgctttgcg cttgaaggac taatcacaag ttcttgaaga tatggaccta ggggagctat 1831
tgcgccacga caggaggaag ttctcagatg ttgcattgat gtaacattgt tgcatttctt 1891
taatgagctg ggctccttcc tcatgtgctt ccaaagaga ttttgtccca ctaatggtgt 1951
gcccatcacc cacactatga aagtaaaagg gatgctgagc agatacagcg tgcttacctc 2011
tcagccatga ctttcatgct attaaaagaa tgcattgtgaa 2051

<210> 4
<211> 196
<212> PRT
<213> Mus musculus

<400> 4
Met Ser Gln Gly Leu Gln Leu Leu Phe Leu Gly Cys Ala Cys Ser Leu
1 5 10 15
Ala Pro Ala Met Ala Met Arg Glu Val Thr Val Ala Cys Ser Glu Thr
20 25 30
Ala Asp Leu Pro Cys Thr Ala Pro Trp Asp Pro Gln Leu Ser Tyr Ala
35 40 45
Val Ser Trp Ala Lys Val Ser Glu Ser Gly Thr Glu Ser Val Glu Leu
50 55 60
Pro Glu Ser Lys Gln Asn Ser Ser Phe Glu Ala Pro Arg Arg Arg Ala

Sequence Listing

65	70	75	80
Tyr Ser Leu Thr Ile Gln Asn Thr Thr Ile Cys Ser Ser Gly Thr Tyr	85	90	95
Arg Cys Ala Leu Gln Glu Leu Gly Gly Gln Arg Asn Leu Ser Gly Thr	100	105	110
Val Val Leu Lys Val Thr Gly Cys Pro Lys Glu Ala Thr Glu Ser Thr	115	120	125
Phe Arg Lys Tyr Arg Ala Glu Ala Val Leu Leu Phe Ser Leu Val Val	130	135	140
Phe Tyr Leu Thr Leu Ile Ile Phe Thr Cys Lys Phe Ala Arg Leu Gln	145	150	155
Ser Ile Phe Pro Asp Ile Ser Lys Pro Gly Thr Glu Gln Ala Phe Leu	165	170	175
Pro Val Thr Ser Pro Ser Lys His Leu Gly Pro Val Thr Leu Pro Lys	180	185	190
Thr Glu Thr Val	195		

<210> 5
 <211> 31
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Description of Artificial Sequence: primer for CD83ext

<400> 5
 tcccccgagg acgccggagg tgaaggtggc t 31

<210> 6
 <211> 31
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Description of Artificial Sequence: primer for CD83ext

<400> 6
 aattagaatt ctcaaattctc cgctctgtat t 31

<210> 7
 <211> 435
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Description of Artificial Sequence: partial
 sequence of pGEX2ThCD83ext
 <220>
 <221> CDS
 <222> (1)..(417)
 <220>
 <221> mat_peptide
 <222> (28)..(417)

Sequence Listing

<400> 7
cct cca aaa tcg gat ctg gtt ccg cgt gga tcc ccg gga acg ccg gag 48
Pro Pro Lys Ser Asp Leu Val Pro Arg Gly Ser Pro Gly Thr Pro Glu
-5 -1 1 5
gtg aag gtg gct tgc tcc gaa gat gtg gac ttg ccc tgc acc gcc ccc 96
Val Lys Val Ala Cys Ser Glu Asp Val Asp Leu Pro Cys Thr Ala Pro
10 15 20
tgg gat ccg cag gtt ccc tac acg gtc tcc tgg gtc aag tta ttg gag 144
Trp Asp Pro Gln Val Pro Tyr Thr Val Ser Trp Val Lys Leu Leu Glu
25 30 35
ggg ggt gaa gag agg atg gag aca ccc cag gaa gac cac ctc agg gga 192
Gly Gly Glu Glu Arg Met Glu Thr Pro Gln Glu Asp His Leu Arg Gly
40 45 50 55
cag cac tat cat cag aag ggg caa aat ggt tct ttc gac gcc ccc aat 240
Gln His Tyr His Gln Lys Gly Gln Asn Gly Ser Phe Asp Ala Pro Asn
60 65 70
gaa agg ccc tat tcc ctg aag atc cga aac act acc agc tgc aac tcg 288
Glu Arg Pro Tyr Ser Leu Lys Ile Arg Asn Thr Thr Ser Cys Asn Ser
75 80 85
ggg aca tac agg tgc act ctg cag gac ccg gat ggg cag aga aac cta 336
Gly Thr Tyr Arg Cys Thr Leu Gln Asp Pro Asp Gly Gln Arg Asn Leu
90 95 100
agt ggc aag gtg atc ttg aga gtg aca gga tgc cct gca cag cgt aaa 384
Ser Gly Lys Val Ile Leu Arg Val Thr Gly Cys Pro Ala Gln Arg Lys
105 110 115
gaa gag act ttt aag aaa tac aga gcg gag att tgagaattca tcgtgact 435
Glu Glu Thr Phe Lys Lys Tyr Arg Ala Glu Ile
120 125 130

<210> 8
<211> 139
<212> PRT
<213> Artificial Sequence
<223> Description of Artificial Sequence: partial
sequence of pGEX2ThCD83ext

<400> 8
Pro Pro Lys Ser Asp Leu Val Pro Arg Gly Ser Pro Gly Thr Pro Glu
-5 -1 1 5
Val Lys Val Ala Cys Ser Glu Asp Val Asp Leu Pro Cys Thr Ala Pro
10 15 20
Trp Asp Pro Gln Val Pro Tyr Thr Val Ser Trp Val Lys Leu Leu Glu
25 30 35
Gly Gly Glu Glu Arg Met Glu Thr Pro Gln Glu Asp His Leu Arg Gly
40 45 50 55
Gln His Tyr His Gln Lys Gly Gln Asn Gly Ser Phe Asp Ala Pro Asn
60 65 70
Glu Arg Pro Tyr Ser Leu Lys Ile Arg Asn Thr Thr Ser Cys Asn Ser
75 80 85

Sequence Listing

Gly Thr Tyr Arg Cys Thr Leu Gln Asp Pro Asp Gly Gln Arg Asn Leu
90 95 100
Ser Gly Lys Val Ile Leu Arg Val Thr Gly Cys Pro Ala Gln Arg Lys
105 110 115
Glu Glu Thr Phe Lys Lys Tyr Arg Ala Glu Ile
120 125 130

<210> 9
<211> 435
<212> DNA
<213> Artificial Sequence
<220>
<223> Description of Artificial Sequence: partial
sequence of pGEX2ThCD83ext_mut129_CtoS
<220>
<221> CDS
<222> (1)..(417)
<220>
<221> mat_peptide
<222> (28)..(417)

<400> 9
cct cca aaa tcg gat ctg gtt ccg cgt gga tcc ccg gga acg ccg gag 48
Pro Pro Lys Ser Asp -5 Leu Val Pro Arg Gly 1 Ser Pro Gly Thr Pro Glu
gtg aag gtg gct tgc tcc gaa gat gtg gac ttg ccc tgc acc gcc ccc 96
Val Lys Val Ala Cys Ser Glu Asp Val Asp Leu Pro Cys Thr Ala Pro
10 15 20
tgg gat ccg cag gtt ccc tac acg gtc tcc tgg gtc aag tta ttg gag 144
Trp Asp Pro Gln Val Pro Tyr Thr Val Ser Trp Val Lys Leu Leu Glu
25 30 35
ggg ggt gaa gag agg atg gag aca ccc cag gaa gac cac ctc agg gga 192
Gly Gly Glu Glu Arg Met Glu Thr Pro Gln Glu Asp His Leu Arg Gly
40 45 50 55
cag cac tat cat cag aag ggg caa aat ggt tct ttc gac gcc ccc aat 240
Gln His Tyr His Gln Lys Gly Gln Asn Gly Ser Phe Asp Ala Pro Asn
60 65 70
gaa agg ccc tat tcc ctg aag atc cga aac act acc agc tgc aac tcg 288
Glu Arg Pro Tyr Ser Leu Lys Ile Arg Asn Thr Thr Ser Cys Asn Ser
75 80 85
ggg aca tac agg tgc act ctg cag gac ccg gat ggg cag aga aac cta 336
Gly Thr Tyr Arg Cys Thr Leu Gln Asp Pro Asp Gly Gln Arg Asn Leu
90 95 100
agt ggc aag gtg atc ttg aga gtg aca gga tcc cct gca cag cgt aaa 384
Ser Gly Lys Val Ile Leu Arg Val Thr Gly Ser Pro Ala Gln Arg Lys
105 110 115
gaa gag act ttt aag aaa tac aga gcg gag att tgagaattca tcgtgact 435
Glu Glu Thr Phe Lys Lys Tyr Arg Ala Glu Ile
120 125 130

Sequence Listing

```

<210> 10
<211> 139
<212> PRT
<213> Artificial Sequence
<223> Description of Artificial Sequence: partial
        sequence of pGEX2ThCD83ext_mut129_CtoS

<400> 10
Pro Pro Lys Ser Asp Leu Val Pro Arg Gly Ser Pro Gly Thr Pro Glu
        -5          -1  1          5
Val Lys Val Ala Cys Ser Glu Asp Val Asp Leu Pro Cys Thr Ala Pro
        10          15          20
Trp Asp Pro Gln Val Pro Tyr Thr Val Ser Trp Val Lys Leu Leu Glu
        25          30          35
Gly Gly Glu Glu Arg Met Glu Thr Pro Gln Glu Asp His Leu Arg Gly
        40          45          50          55
Gln His Tyr His Gln Lys Gly Gln Asn Gly Ser Phe Asp Ala Pro Asn
        60          65          70
Glu Arg Pro Tyr Ser Leu Lys Ile Arg Asn Thr Thr Ser Cys Asn Ser
        75          80          85
Gly Thr Tyr Arg Cys Thr Leu Gln Asp Pro Asp Gly Gln Arg Asn Leu
        90          95          100
Ser Gly Lys Val Ile Leu Arg Val Thr Gly Ser Pro Ala Gln Arg Lys
        105          110          115
Glu Glu Thr Phe Lys Lys Tyr Arg Ala Glu Ile
        120          125          130

<210> 11
<211> 32
<212> DNA
<213> Artificial Sequence
<220>
<223> Description of Artificial Sequence: primer
        sense-pGEX2ThCD83

<400> 11
tccccccggg aacgccggag gtgaaggtgg ct 32

<210> 12
<211> 66
<212> DNA
<213> Artificial Sequence
<220>
<223> Description of Artificial Sequence: primer
        antisense-CD83extra_mutantCtoS

<400> 12
aattagaatt ctcaaatctc cgctctgtat ttcttaaaag tctcttcttt acgctgtgca 60
ggggat 66

```

<210> 13

Sequence Listing

<211> 209

<212> PRT

<213> Homo sapiens

<400> 13

```

Gly Ser Pro Gly Met Ser Arg Gly Leu Gln Leu Leu Leu Leu Ser Cys
1      5      10      15
Ala Tyr Ser Leu Ala Pro Ala Thr Pro Glu Val Lys Val Ala Cys Ser
      20      25      30
Glu Asp Val Asp Leu Pro Cys Thr Ala Pro Trp Asp Pro Gln Val Pro
      35      40      45
Tyr Thr Val Ser Trp Val Lys Leu Leu Glu Gly Gly Glu Glu Arg Met
      50      55      60
Glu Thr Pro Gln Glu Asp His Leu Arg Gly Gln His Tyr His Gln Lys
65      70      75      80
Gly Gln Asn Gly Ser Phe Asp Ala Pro Asn Glu Arg Pro Tyr Ser Leu
      85      90      95
Lys Ile Arg Asn Thr Thr Ser Cys Asn Ser Gly Thr Tyr Arg Cys Thr
      100      105      110
Leu Gln Asp Pro Asp Gly Gln Arg Asn Leu Ser Gly Lys Val Ile Leu
      115      120      125
Arg Val Thr Gly Cys Pro Ala Gln Arg Lys Glu Glu Thr Phe Lys Lys
      130      135      140
Arg Arg Ala Glu Ile Val Leu Leu Leu Ala Leu Val Ile Phe Tyr Leu
145      150      155      160
Thr Leu Ile Ile Phe Thr Cys Lys Phe Ala Arg Leu Gln Ser Ile Phe
      165      170      175
Pro Asp Phe Ser Lys Ala Gly Met Glu Arg Ala Phe Leu Pro Val Thr
      180      185      190
Ser Pro Asn Lys His Leu Gly Leu Val Thr Pro His Lys Thr Glu Leu
      195      200      205
Val
209

```